

Gencore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 24, 1999, 01:30:01 ; Search time 366.45 Seconds
(without alignments)
1435.120 Million cell updates/sec

Title: US-09-205-015-2
Perfect score: 147
Sequence: 1 agataactggccaaaccatg.....cctcccccactgtttatct 147

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

Database : GenEmbl:
1: gb_ba1: *
2: gb_ba2: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_dat: *
7: gb_ph: *
8: gb_dll1: *
9: gb_dl2: *
10: gb_pr1: *
11: gb_pr2: *
12: gb_pr3: *
13: gb_ro: *
14: gb_st: *
15: gb_sy: *
16: gb_un: *
17: gb_v1: *
18: gb_htg: *
19: em_ba: *
20: em_fun: *
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22: em_hum2: *
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24: em_om: *
25: em_or: *
26: em_ov: *
27: em_pat: *
28: em_ph: *
29: em_pl: *
30: em_ro: *
31: em_sy: *
32: em_un: *
33: em_v1: *
34: em_htg: *
35: em_sts: *
36: gb_ba1: *
37: gb_ba2: *
38: gb_p11: *
39: gb_p12: *
40: gb_pr1: *
41: gb_pr2: *
42: gb_pr3: *
43: gb_sts: *

ALIGNMENTS

RESULT 1

LOCUS S49899 356 bp DNA PRI
DEFINITION alpha-globin gene cluster; [5' region, major regulatory element]
[Human, Genomic, 356 nt].
ACCESSION S49899
NID 9233377
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE

AUTHORS Jarman,A.P., Wood,W.G., Sharpe,J.A., Gourdon,G., Ayyub,H. and
Higgs,D.R.

TITLE Characterization of the major regulatory element upstream of the
human alpha-globin gene cluster
JOURNAL Mol. Cell. Biol. 11 (9), 4679-4689 (1991)

REMARK

GenBank staff at the National Library of Medicine created this
entry [NCBI gbbg 49899] from the original journal article.
This sequence comes from fig 5.
Region: alpha-globin gene cluster

SUMMARIES

Result % Query Score Match Length DB ID Description
No. -

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S49899	LOCUS	S49899	356 bp	DNA	PRI	10-JUL-1992	GG4 came from the Los Alamos, flow sorted human Chromosome 16 library.
DEFINITION		alpha-globin gene cluster: [5' region, major regulatory element]			FEATURES		Location/Qualifiers
ACCESSION		[human, Genomic, 356 nt].			SOURCE		1. .19226
NID	S49899						/organism="Homo sapiens"
KEYWORDS	923377						/db_xref="taxon:9606"
SOURCE	human.						/chromosome="16"
ORGANISM	Homo sapiens						/map="16p13.3"
REFERENCE	Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 355)						/clone="SG4"
AUTHORS	Jarman,A.P., Wood,W.G., Sharpe,J.A., Gourdon,G., Ayyub,H. and Higgs,D.R.						repeat_region
TITLE	Characterization of the major regulatory element upstream of the human alpha-globin gene cluster						/note="AluJb repeat: matches 301. .5 of consensus"
JOURNAL	Mol. Cell. Biol. 11 (9), 4679-4689 (1991)						repeat_region
MEDLINE	91342671						1156. .1290
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gibbog 49899] from the original journal article. This sequence comes from fig 5.						/note="AluSx repeat: matches 1. .136 of consensus"; incomplete repeat"
COMMENT	Region: alpha-globin gene cluster.						1291. .1601
FEATURES	Location/Qualifiers						/note="AluSp repeat: matches 1. .300 of consensus"
source	1. .356						1602. .1758
	/organism="Homo sapiens"						/note="AluSg repeat: matches 132. .288 of consensus"; incomplete repeat"
	/db_xref="taxon:9606"						3487. .3784
BASE COUNT	89 a 89 c 108 g 70 t						/note="AluSg repeat: matches 1. .299 of consensus"
ORIGIN							3809. .4104
							/note="AluJg repeat: matches 1. .302 of consensus"
							4823. .5030
							/note="AluSg repeat: matches 2. .208 of consensus"; incomplete repeat"
							5053. .5092
							/note="20 copies of 2 mer 85 % conserved"
							5122. .5280
							/note="FAM repeat: matches 164. .5 of consensus"
							5759. .5903
							/note="LMC2 repeat: matches 169. .321 of consensus"
							6130. .6427
							/note="AluSg repeat: matches 297. .1 of consensus"
							6428. .6724
							/note="AluJg repeat: matches 299. .1 of consensus"
							7144. .7265
							/note="LMC2 repeat: matches 293. .159 of consensus"
							7453. .7747
							/note="AluSp repeat: matches 1. .303 of consensus"; CDS complement(join(7979. .8064,10081. .10234,147660. .14834,165681. .166682))
							/codon_start=1
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							/db_xref="PID:e300374"
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							LFENYVFLARANADPSPEFHILPCKLARDLKEYLDR"
RESULT	4						repeat_region
HSGG4	LOCUS	HSGG4	19226 bp	DNA	PRI	19-MAR-1997	repeat_region
DEFINITION		Human DNA sequence from cosmid GG4 from a contig from the tip of the short arm of chromosome 16, spanning 2mb of 16p13.3.					repeat_region
ACCESSION	284722						284722. .8307
NID	91817579						/note="AluSg repeat: matches 212. .1 of consensus"; incomplete repeat"
KEYWORDS	16p13.3.						8578. .8861
SOURCE	human.						/note="Alu repeat: matches 3. .297 of consensus"
ORGANISM	Homo sapiens						8907. .9210
REFERENCE	Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.						/note="AluJb repeat: matches 300. .1 of consensus"
AUTHORS	Flint,J. and Higgs,D.R.						repeat_region
TITLE	Direct Submission						12438. .12731
JOURNAL	Submitted (28-JAN-1997) Sanger Centre, 970124/Hinxton, Cambridgeshire, CB10 1RQ, UK. E-mail enquires: humpub@sanger.ac.uk						/note="Alu repeat: matches 105. .185 of consensus"; incomplete repeat"
COMMENT	IMPORTANT: This sequence is not the entire insert of clone GG4. This clone was sequenced at the Institute of Molecular Medicine. The true left end of clone GG4 is at 1 in this sequence. The true right end of clone R36 is at 456. The true left end of clone P394 is at 19090.						14140. .14453
	16p.						/note="AluSx repeat: matches 1. .302 of consensus"
	Higgs,D.R., Flint,J. unpublished. MRC Molecular Haematology Unit, Institute of Molecular Medicine, Oxford.						/note="AluSp repeat: matches 760. .907 of consensus"
							16385. .16584
							/note="10 copies of 20 mer 91 % conserved"
							18800. .19099
							/note="AluSx repeat: matches 1. .293 of consensus"

chromosome 6q12-q13
 Genomics 41 (2), 236-242 (1997)
 MEDLINE
 2 (bases 1 to 9750)
 REFERENCES
 AUTHORS
 Olson, P.
 TITLE
 Direct Submission
 Submitted (09-OCT-1996) Cutaneous Biology Research Center, Thirteenth
 Massachusetts General Hospital, Third floor, Bldg.149, Thirteenth
 St., Charlestown, MA 02129, USA
 JOURNALS
 FEATURES
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 5' UTR
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 CDS
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 /ab_xref="taxon:3606"
 /chromosome="6"
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 keratinocytes; squamous cell carcinoma cells; endothelial
 (HUVEC) cell lines"
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 114. .185
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 114. .9105
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 TGAIDVYKVNTTEASAGARVEPKVYALIITDGKSQDVEFEPAREKRNVEVSIGI
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 FVQ1SDEKSEKSFQKUNTYNDKALQVYDQKPKVYDQKPKVYDQKPKVYDQKPK
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 GVSLESGGSSPSYSAVQ1SNEQPTADLHPKPPY1TLLFPLPPEPSDFPKVYDQKPK
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to AA009412 ze82h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5'. (62. .144); 100% identity."

repeat_region

misc_feature

/note="DBS similarity to AA136115 zk90b04.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490033 5' (193. .394); 94% identity.--DBS similarity to AA009412 ze82h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5'. (145. .346); 96% identity.--(11121. .11331) DDS similarity to AA009693 ze82h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 3' (429. .307); 95% identity.--(11127. .11246) DDS similarity to AA047548 zf15e02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 377018 5' (2222. .341); 97% identity.--(11061. .11131) predicted exon, program: grail2exons_human_1.3, frame: 0, quality: good, score: 73.000--(11061. .11120) DDS similarity to AA451628 zx33f04.rl Soares total fetus Nb2HP8 9w Homo sapiens cDNA clone 788287 5' (167. .313); 98% identity."

repeat_region

misc_feature

/note="DBS similarity to AA136115 zk90b04.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490033 5' (395. .477); 92% identity.--DBS similarity to AA009412 ze82h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5' (347. .427); 94% identity.--DBS similarity to AA009693 ze82h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 3' (306. .228); 99% identity.--DBS similarity to AA451601 zx33f04.rl Soares total fetus Nb2HP8 9w Homo sapiens cDNA clone 788287 3' (309. .229); 99% identity.--"

repeat_region

misc_feature

/note="DBS similarity to AA136115 zk90b04.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490033 5' (1250. .12581); 92% identity."

repeat_region

misc_feature

/note="DBS similarity to AA136115 zk90b04.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490033 5' (1250. .12581); 92% identity.--DBS similarity to AA009412 ze82h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5' (347. .427); 94% identity.--DBS similarity to AA009693 ze82h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 3' (306. .228); 99% identity.--DBS similarity to AA451601 zx33f04.rl Soares total fetus Nb2HP8 9w Homo sapiens cDNA clone 788287 3' (309. .229); 99% identity.--"

repeat_region

misc_feature

/note="DBS similarity to AA13756. .14029) complement(13274. .13531) /rpt.family="Ali"

repeat_region

misc_feature

/note="predicted exon, program: grail2exons human_1.3, frame: 2, quality: good, score: 61.000--Other overlapping matches:--(13756. .13984) DDS similarity to AA05010 2x33f04.rl Soares total fetus Nb2HP8 9w Homo sapiens cDNA clone 788287 3' (228. .1); 99% identity.--"

repeat_region

misc_feature

/note="DBS similarity to AA13756. .14029) complement(13274. .13531) /rpt.family="Ali"

repeat_region

misc_feature

/note="DBS similarity to AA13756. .14029) complement(13274. .13531) /rpt.family="Ali"

repeat_region

misc_feature

/note="DBS similarity to AA406406 zv11e07.s1 Soares NbHPU S1 Homo sapiens cDNA clone 753348 3', (1. .433); score: 858 Identity: 431/433 (99%) ---(13756. .13984) DDS similarity to W3715_zb21a02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 302666 5' (..-.355); 94% identity.--(15227. .14885) DDS similarity to AA121532 zk89c11.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490004 3' (342. .1); 99% identity.--(15227. .14885) DDS similarity to AA121532 zk89c11.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490004 5' (126. .467); 99% identity.--(15227. .14897) DDS similarity to W46603 zk32h10.rl Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067 5' (328. .1); 98% identity.--(15227. .15088) DDS similarity to W46604 zk32h10.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067 3' (322. .465); 96% identity."

repeat_region

misc_feature

/note="DBS similarity to AA121532 zk89c11.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490004 3' (389. .343); 99% identity.--DBS similarity to AA17694 zk89c11.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490004 5' (77. .125); 90% identity.--(15735. .15713) DDS similarity to W46603 zk32h10.rl Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067 5' (448. .352); 97% identity.--(21268) DDS similarity to W46604 identity.--(21494. .21268) DDS similarity to W46604 complement(21209. .21494) /rpt.family="Ali"

repeat_region

misc_feature

/note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 94.000--Other overlapping matches:--(21494. .21213) DDS similarity to AA049280 m45d02.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to SW:IL6_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (104. .273); 86% identity.--(20245. .20080) DDS similarity to W66776 me17b1.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to SW:IL6_MOUSE (274. .431); 93% identity.--"

repeat_region

misc_feature

/note="predicted exon, program: grail2exons_human_1.3, frame: 2, quality: excellent, score: 100.000--DBS similarity to AA049280 m45d02.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to SW:IL6_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (316. .158); 92% identity.--"

repeat_region

misc_feature

/note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 100.000--DBS similarity to AA049280 m45d02.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to SW:IL6_MOUSE (316. .158); 92% identity.--"

repeat_region

misc_feature

/note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 100.000--DBS similarity to AA049280 m45d02.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to SW:IL6_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (104. .273); 86% identity.--(20245. .20080) DDS similarity to W66776 me17b1.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to SW:IL6_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (104. .273); 86% identity.--(20245. .20080) DDS similarity to W66776 me17b1.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to SW:IL6_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (316. .158); 92% identity.--"

repeat_region

misc_feature

/note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 100.000--DBS similarity to AA049280 m45d02.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to SW:IL6_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (316. .158); 92% identity.--"

repeat_region

misc_feature

/note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 100.000--DBS similarity to AA049280 m45d02.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to SW:IL6_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (316. .158); 92% identity.--"

repeat_region

misc_feature

/note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 100.000--DBS similarity to AA049280 m45d02.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to SW:IL6_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (316. .158); 92% identity.--"

repeat_region

misc_feature

/note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 100.000--DBS similarity to AA049280 m45d02.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to SW:IL6_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (316. .158); 92% identity.--"

mailto:egreen@hgri.nih.gov

SOURCE INFORMATION:
 Clone RG167B05 is from the first release of the human BAC library
 C1TB-978SK-B. The library contains cloned DNA from the male
 fibroblast cell line 978SK. See: Shizuya et al., Proc. Natl.
 Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8
 (1996). This clone is available from Research Genetics, Inc.
 (<http://www.resgen.com>).

VECTOR: pBeloBAC11

Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:
 The actual start of this clone is at base position 1 of RG167B05;
 the actual end of this clone is at base position 118313 of RG167B05.

This clone contains SRS SWS2908 (NID:91113638.

FEATURES

source	repeat_region
1. 1118313	repeat_region
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/map="7q11"	repeat_region
353 . 519	repeat_region
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527 . 626	repeat_region
/rpt_family="MER1-type"	repeat_region
686 . 832	repeat_region
/rpt_family="MER1-type"	repeat_region
914 . 999	repeat_region
/rpt_family="L1.2"	repeat_region
1073 . 1117	repeat_region
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159 . 1503	repeat_region
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3917 . 4205	repeat_region
/rpt_family="Alu"	repeat_region
4701 . 4855	repeat_region
/rpt_family="Alu"	repeat_region
/gene="SRX"	repeat_region
complement(join(<5050. .7954))	repeat_region
/gene="SRX"	repeat_region
H RG167B05.1"	repeat_region
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/product="calcium binding protein amplified in multidrug resistant cells"	repeat_region
/db_xref="PID:9277236"	repeat_region
/translation="MAYPGPGAGGGYPGGGAPGPPGQTQDPPLYGTAAVAG QDGQDADEPORCLTQSGLGGYK"	repeat_region
9625 . 10516	repeat_region
/rpt_family="L1"	repeat_region
10518 . 11038	repeat_region
/rpt_family="L1"	repeat_region
11200 . 11288	repeat_region
/rpt_family="MIR"	repeat_region
11353 . 11404	repeat_region
/rpt_family="MER1-type"	repeat_region
11466 . 11711	repeat_region
/rpt_family="MER1-type"	repeat_region
12803 . 12113	repeat_region
/rpt_family="MER1-type"	repeat_region
13488 . 13127	repeat_region
/rpt_family="MIR"	repeat_region
15273 . 15566	repeat_region
/rpt_family="Alu"	repeat_region
15767 . 15829	repeat_region
/rpt_family="MER1-type?"	repeat_region
15947 . 16238	repeat_region
/rpt_family="Alu"	repeat_region

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repeat_region          38570 . 38737
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repeat_region          38746 . 40503
/rpt_family="Alu"
repeat_region          4050 . 40560
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repeat_region          40573 . 40874
/rpt_family="Alu"
repeat_region          40945 . 41237
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repeat_region          41457 . 42699
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repeat_region          43683 . 44216
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repeat_region          4433 . 44975
/rpt_family="L1"
repeat_region          45663 . 46301
/rpt_family="L2"
repeat_region          46475 . 46665
/rpt_family="Alu"
repeat_region          46691 . 46867
/rpt_family="Alu"
repeat_region          46875 . 47123
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repeat_region          47148 . 47453
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repeat_region          47465 . 47723
/rpt_family="L2"
repeat_region          4894 . .49001
/rpt_family="MIR"
repeat_region          49438 . 49710
/rpt_family="Alu"
repeat_region          50605 . 50902
/rpt_family="Alu"
repeat_region          50923 . 51302
/rpt_family="L1"
repeat_region          51531 . 51683
/rpt_family="MER1-type"
repeat_region          51858 . 52279
/rpt_family="L1"
repeat_region          52333 . 52634
/rpt_family="L1"
repeat_region          52761 . 5284
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repeat_region          53422 . 53408
/rpt_family="SVA"
repeat_region          53986 . 55215
/rnote="CPG_Island (%GC=72.8, o/e=0.70, #CPGs=95)"
repeat_region          56698 . 56786
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repeat_region          57713 . 57791
/rpt_family="MIR"
repeat_region          58071 . 58124
/rpt_family="L1"
repeat_region          58849 . 59127
/rpt_family="L1"
repeat_region          59146 . 59176
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repeat_region          59317 . 59874
/rpt_family="L1"
repeat_region          60088 . 60425
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repeat_region          60906 . 61152
/rpt_family="L1"
repeat_region          61996 . 62123
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repeat_region          62445 . 63016
/rpt_family="MER4-group"
repeat_region          63017 . 63319
/rpt_family="Alu"
repeat_region          63321 . 63385
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repeat_region          64977 . 65009
/complement("64937") (NID:9783370) yh53a03.r1"
repeat_region          65019 . 65370
/complement("65019") (NID:9783370) yh53a03.r1"
repeat_region          65370 . 65237
/complement("65370") (NID:9783370) yh53a03.r1"
repeat_region          65522 . 65805
/note="match to EST R2735 (NID:9783370) yh53a03.r1"
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repeat_region          68396 . 68360
/rpt_family="MER1-type"
repeat_region          70076 . 70373
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repeat_region          70374 . 70469
/note="match to EST AA244027 (NID:91874750) nc04a09.r1"
repeat_region          71252 . 71561
/complement("71252") (NID:9666875)
repeat_region          72533 . 73353
/note="match to EST (NID:9666875)"
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repeat_region          73841 . 73890
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repeat_region          73904 . 74470
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repeat_region          74471 . 74638
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repeat_region          74882 . 74743
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repeat_region          75310 . 76002
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repeat_region          76597 . 76396
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repeat_region          76517 . 76788
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repeat_region          77027 . 77111
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repeat_region          78203 . 78305
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repeat_region          78316 . 78394
/rpt_family="MER84"
repeat_region          78398 . 78897
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repeat_region          79487 . 79434
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repeat_region          80384 . 81898
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repeat_region          82043 . 82107
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repeat_region          85398 . 85585
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repeat_region          85709 . 86050
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repeat_region          86395 . 86438
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/rpt_family="Alu"
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/rpt_family="Alu"
repeat_region          88530 . 88642
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repeat_region          89216 . 89504
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